REMARKS/ARGUMENTS

The claims have been amended to address a formality. Specifically, the claims no longer recited the non-elected sequences. No new matter has been added.

Withdrawal of the objection to the claims for reciting non-elected sequences is respectfully requested in view of the above-amendment to the claims.

Claims 1-4, 6, 8, 14 and 15 were rejected under 35 USC §112, first paragraph, as failing to comply with the written description requirement. It is stated on page 3 of the Office Action that "given the lack or written description in the specification with regard to the structural and physical characteristics of the claimed compositions, one skilled in the art would not have been in possession of the genus claimed at the time this application was filed."

Attention is kindly invited to Example 10 which is set forth on pages 44-45 of the instant specification. It is stated on page 44 at lines 19-25 that

> The two soybean delta-9 desaturase genes previously identified, designated pDS 1 and 2 (US Pat Nos. 5,443,974 and 5,760,206) share a high degree of homology to other known delta-9 desaturase genes such as castor and safflower (US Pat No. 5,723,595). The genes of the present invention have less than 65% amino acid sequence identity to these previously described plant delta-9 desaturase polypeptides. All of the soybean delta-9 desaturase genes were placed into E. coli and shown to have delta-9 desaturase activity. . . .

The results presented in Table 10 (Example 10) confirmed that the diverged delta-9 desaturase sequences do encode functional enzymes. It is further stated on page 45 at lines 21-28 that

> These results confirm that the diverged delta-9 desaturase sequences do encode functional enzymes. Furthermore, pDS3 may be the dominant activity found in soybeans. The conserved sequence elements KEIPDDYFVVLVGDMITEEALPTYQTMLNT corresponding to positions 116-145 of SEQ ID NO:23; and DYADILEFLVGRWK corresponding to positions 324-337 of SEQ ID NO:23 from the Thompson patent (US Patent No. 5,723,595) that are claimed to be indicative of delta-9 desaturases are not conserved in the diverged sequences of the instant invention. Therefore, the sequences of the instant invention define a new functional class of plant delta-9 desaturase genes.

It is clear from the foregoing that even though the diverged sequences of the instant invention do not appear to share conserved sequence elements that are associated with delta-9 desaturase activity, nevertheless, the claimed sequences do indeed possess delta-9 desaturase activity. Thus, the claimed sequences appear to define a new functional class of plant delta-9 desaturases.

In view of the foregoing discussion, it is respectfully submitted that the written description is satisfied.

Accordingly, withdrawal of the rejection of the claims under 35 USC §112, first paragraph, is respectfully requested.

Claims 1-9, 14 and 15 were rejected under 35 USC §112, first paragraph, as failing to comply with the enablement requirement.

pDS1 and pDS2 were constructed using two delta-9 soybean genes previously identified (US Patent Nos. 5,443,974 and 5,760,206). These gense share a high degree of homology to other known delta-9 desaturase genes such as castor and safflower (US Patent No. 5,723,595).

pDS3 was constructed using SEQ ID NO:1. Specifically, nucleotides 6054-6611 linked to 1-411 of SEQ ID NO: 26 (as stated on page 45, line 4 of the specification) correspond to nucleotides 326-1289 of SEQ ID NO:1. Appendix A submitted herewith sets forth an alignment of SEQ ID NO:1 and SEQ ID NO: 26 to show that SEQ ID NO:26 which is the sequence for pBS68 comprises the sequence set forth in SEQ ID NO:1.

Thus, the specification does provide guidance with regard to evaluating plants transformed with any of the claimed sequences, and there is guidance with regard to evaluating the expression of diverged delta-9 stearoyl fatty acid desaturases in host cells or plants.

Applicants are not relying on sequence identity of DNA or amino acid sequences in identifying related sequences encoding enzymes having a particular activity. Indeed, the sequences of the instant invention are shown in Example 10 as having delta-9 desaturase activity.

Attention is kindly invited to Table 5 on page 32 that sets forth percent identity of polypeptides homologous to a diverged delta-9, or stearoyl-ACP, desaturase.

It is respectfully submitted that one skilled in the art can make and use the invention as broadly claimed without engaging in undue experimentation.

Accordingly, withdrawal of the rejection of the claims under 35 USC §112, first paragraph, is respectfully requested.

Claims 1-3, 6 and 8 were rejected under 35 USC §102(a) as being anticipated by Swiderski et al. (Plant Science 151:75-83, 2000 in IDS, see alignment AF139377, March 17, 2000). It is stated on page 7 of the Office Action that "Swiderski et al teach a nucleic acid sequence encoding a polypeptide having at least 90% identity to SEQ ID NO:2, and said clone in a cDNA library would require the sequence in a construct and a host cell."

Claim 1 recites an isolated polynucleotide comprising:

(a) a nucleotide sequence encoding a polypeptide having delta-9 fatty acid desaturase activity that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO:2; or

(b) the complement of (a).

Attention is kindly invited to Table 5 on page 32. When SEQ ID NO:2 is compared to the sequence of Swiderski et al., (AF139377 discloses the lupine nucleotide sequence and gi 4704824 corresponds to the encoded protein sequence, see FEATURES section of the Swiderski reference in the Result 3 alignment supplied with the Office Action which shows that AF139377 and gi 470824 refer to the same sequence), identified as gi 4704824 (SEQ ID NO:17), using the Clustal method of alignment the percent identity is 77.6%, not the 90% mentioned on page 7 of the Office Action.

Submitted herewith as Appendix B is a percent identity table for the sequence alignment set forth in Figure 1. The results set forth in Appendix B were obtained using the Clustal method of alignment. Appendix B also shows that AF138377 and gi 4704824 have 100% sequence identity.

Thus, it is respectfully submitted that Siwderski et al. do not anticipate the claimed invention. Withdrawal of the rejection of the claims under 35 USC §102(a) as being anticipated by Swiderski et al. is respectfully requested.

Claim 1 was rejected under 35 USC §102(b) as being anticipated by Sato et al. (Plant Physiol. 99:362-363, 1992), Accession M83199. The jojoba (*Simmondsia chinensis*) sequence used in Example 3 of the specification as gi 267036 (SEQ ID NO:20) is the protein translation product of the nucleotide sequence disclosed in M83199.

When SEQ ID NO:2 is compared to the sequence of Sato et al., (identified as gi267036 or M83199 in GenEMBL Accession M83199 dated April 27, 1993 that accompanied the Office Action), using the Clustal method

of alignment the percent identity is 60.1%. Attention is kindly invited to Appendix B which shows that M83199 and gi267036 share 100% percent sequence identity.

Thus, it is respectfully submitted that Sato et al. do not anticipate the claimed invention. Withdrawal of the rejection of the claims under 35 USC §102(b) as being anticipated by Sato et al. is respectfully requested.

In view of the foregoing, it is respectfully submitted that the claims are now in form for allowance which allowance is respectfully requested.

A petition for a three (3) month extension of time accompanies this response.

Please charge any fees or credit any overpayment associated with the filing of this Amendment including, but not limited to the Extension of Time, to Deposit Account No. 04-1928 (E. I. du Pont de Nemours and Company).

Respectfully submitted,

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Dated: January 29, 2004

SID1 vs SID26.txt

SID1: SEQ ID NO:1 nucleotides 326-1289
SID26: SEQ ID NO:26 nucleotides 6054-6611 + 1-411

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SID1    AAAGAAATTTTCAAGTCCTTGGAGGGATGGGCCTCGGAGTGGGTCCTACCGCTGCTGAAG
SID26   AAAGAAATTTTCAAGTCCTTGGAGGGATGGGCCTCGGAGTGGGTCCTACCGCTGCTGAAG

SID1    CCCGTGGAGCAATGCTGGCAGCCACAAAACTTCCTCCCTGACCCCTCCCTTCCGCATGAA
SID26   CCCGTGGAGCAATGCTGGCAGCCACAAAACTTCCTCCCTGACCCCTCCCTTCCGCATGAA

SID1    GAGTTCAGCCATCAGGTGAAGGAGCTTCGCGAACGCACTAAAGAGTTACCTGATGAGTAC
SID26   GAGTTCAGCCATCAGGTGAAGGAGCTTCGCGAACGCACTAAAGAGTTACCTGATGAGTAC

SID1    TTTGTGGTGCTGGTGGGTGATATGGTCACCGAGGACGCGCTTCCCACTTACCAGACCATG
SID26   TTTGTGGTGCTGGTGGGTGATATGGTCACCGAGGACGCGCTTCCCACTTACCAGACCATG

SID1    ATCAACAACCTTGATGGAGTGAAAGATGACAGCGGCACGAGCCCGAGCCCGTGGGCCGTG
SID26   ATCAACAACCTTGATGGAGTGAAAGATGACAGCGGCACGAGCCCGAGCCCGTGGGCCGTG

SID1    TGGACCCGGGCCTGGACCGCCGAGGAAAACAGACACGGGGATCTGCTCAGAACTTATTTG
SID26   TGGACCCGGGCCTGGACCGCCGAGGAAAACAGACACGGGGATCTGCTCAGAACTTATTTG

SID1    TATCTCTCTGGGAGGGTTGACATGGCTAAGGTCGAAAAGACCGTACATTACCTCATTTCA
SID26   TATCTCTCTGGGAGGGTTGACATGGCTAAGGTCGAAAAGACCGTACATTACCTCATTTCA

SID1    GCTGGCATGGACCCTGGGACAGACAACAACCCATATTTGGGGTTTGTGTACACGTCATTC
SID26   GCTGGCATGGACCCTGGGACAGACAACAACCCATATTTGGGGTTTGTGTACACGTCATTC

SID1    CAAGAGCGAGCAACATTTGTGGCGCACGGGAACACGGCTCGGCTCGCGAAGGAGGGCGGG
SID26   CAAGAGCGAGCAACATTTGTGGCGCACGGGAACACGGCTCGGCTCGCGAAGGAGGGCGGG

SID1    GATCCAGTGCTGGCGCGC----CTATGCGGGACCATCGCAGCGGACGAGAAGCGGCACGA
SID26   GATCCAGTGCTGGCGCGCGCGCCTATGCGGGACCATCGCAGCGGACGAGAAGCGGCACGA

SID1    GAACGCGTACTCAAGAATCGTGGAGAAGCTTCTGGAAGTGGACCCCACCGGGGCAATGGT
SID26   GAACGCGTACTCAAGAATCGTGGAGAAGCTTCTGGAAGTGGACCCCACCGGGGCAATGGT

SID1    GGCCATAGGGAACATGATGGAGAAGAAGATCACGATGCCGGCGCACCTTATGTACGATGG
SID26   GGCCATAGGGAACATGATGGAGAAGAAGATCACGATGCCGGCGCACCTTATGTACGATGG

SID1    GGATGACCCCAGGCTATTCGAGCACTACTCCGCTGTGGCGCAGCGCATAGGCGTGTACAC
SID26   GGATGACCCCAGGCTATTCGAGCACTACTCCGCTGTGGCGCAGCGCATAGGCGTGTACAC

SID1    CGCCAACGACTACGCAGACATCTTGGAGTTTCTCGTTGAACGGTGGAGATTGGAGAAGCT
SID26   CGCCAACGACTACGCAGACATCTTGGA-TTTCTCGTTGA-CGGTGAAGATTGGAGAAGCT

SID1    TGAAGGATTGATGGCTGAGGGGAAGCGGGCGC-AGGATTTC-GTGTGTGGGTTGGCGCCG
SID26   TGAAGGATTGATGCCTGAGGGGAAGCGGGCCCCAGGATTTCCGTGTGTGGGTTGCCCCCG

SID1    AGGATTAGGAGGTTGCAAGAACGCGCTGATGAGCGAGCGCGTAAGATGAAGAAGCATCAT
SID26   AGGATTAGGAGGTTCCAAGAACGCGCTGATGAGCGAGCGCGTAAGATGAAGAAGCATCAT

SID1    GGCGTTAAGT
SID26   GCCGTTAAGT
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APPENDIX B

Percent Identity Table for Sequence Alignment Shown in Figure 1
(proteins encoded by AF139377 and M83199 were used in the alignment)

	SID10	SID12	SID14	SID16	4704824	267036	6957724	3355632	SID23	AF139377	M83199	
SID2	44.7	64.2	45.7	63.0	77.6	60.1	54.8	59.3	60.1	77.6	60.1	SID2
SID10	***	53.4	64.4	52.0	45.3	49.2	48.4	49.5	48.3	45.3	49.2	SID10
SID12		***	51.6	85.8	64.2	61.6	60.5	63.2	62.4	64.2	61.6	SID12
SID14			***	49.3	42.5	45.2	50.2	44.3	45.7	42.5	45.2	SID14
SID16				***	64.6	60.4	61.2	64.0	62.7	64.6	60.4	SID16
4704824					***	62.0	56.5	62.0	62.5	100.0	62.0	4704824
267036						***	61.8	76.0	77.5	62.0	100.0	267036
6957724							***	68.2	67.0	56.5	61.8	6957724
3355632								***	78.8	62.0	76.0	3355632
SID23									***	62.5	77.7	SID23
AF139377										***	62.0	AF139377
	SID10	SID12	SID14	SID16	4704824	267036	6957724	3355632	SID23	AF139377	M83199	